

# SEQUENCE LISTING

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Immunex Corporation  
Cornell Research Foundation, Inc.

<120> Methods of Inhibiting Platelet Activation and Recruitment

<130> 23,495 USA

<140> US 09/807,660

<141> 2001-09-06

<150> US 60/104,585

<151> 1998-10-16

<150> US 60/107,466

<151> 1998-11-06

<150> US 60/149,010

<151> 1999-08-13

<160> 37

<170> PatentIn version 3.1

<210> 1

<211> 1599

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (67)..(1596)

<400> 1

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Met Glu Asp Thr Lys Glu Ser Asn Val Lys Thr Phe Cys Ser  
1 5 10

aag aat atc cta gcc atc ctt ggc ttc tcc tct atc ata gct gtg ata 156  
Lys Asn Ile Leu Ala Ile Leu Gly Phe Ser Ser Ile Ile Ala Val Ile  
15 20 25 30

gct ttg ctt gct gtg ggg ttg acc cag aac aaa gca ttg cca gaa aac 204  
Ala Leu Leu Ala Val Gly Leu Thr Gln Asn Lys Ala Leu Pro Glu Asn  
35 40 45

gtt aag tat ggg att gtg ctg gat gcg ggt tct tct cac aca agt tta 252  
Val Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu  
50 55 60

tac atc tat aag tgg cca gca gaa aag gag aat gac aca ggc gtg gtg 300  
Tyr Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val  
65 70 75

cat caa gta gaa gaa tgc agg gtt aaa ggt cct gga atc tca aaa ttt 348  
His Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe  
80 85 90

gtt cag aaa gta aat gaa ata ggc att tac ctg act gat tgc atg gaa 396  
Val Gln Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu  
95 100 105 110

aga Arg	gct Ala	agg Arg	gaa Glu	gtg Val 115	att Ile	cca Pro	agg Arg	tcc Ser	cag Gln 120	cac His	caa Gln	gag Glu	aca Thr	ccc Pro 125	gtt Val	444
tac Tyr	ctg Leu	gga Gly	gcc Ala 130	acg Thr	gca Ala	ggc Gly	atg Met	cgg Arg 135	ttg Leu	ctc Leu	agg Arg	atg Met	gaa Glu 140	agt Ser	gaa Glu	492
gag Glu	ttg Leu	gca Ala 145	gac Asp	agg Arg	gtt Val	ctg Leu	gat Asp 150	gtg Val	gtg Val	gag Glu	agg Arg	agc Ser 155	ctc Leu	agc Ser	aac Asn	540
tac Tyr	ccc Pro 160	ttt Phe	gac Asp	ttc Phe	cag Gln	ggg Gly 165	gcc Ala	agg Arg	atc Ile	att Ile	act Thr 170	ggc Gly	caa Gln	gag Glu	gaa Glu	588
ggt Gly 175	gcc Ala	tat Tyr	ggc Gly	tgg Trp	att Ile 180	act Thr	atc Ile	aac Asn	tat Tyr	ctg Leu 185	ctg Leu	ggc Gly	aaa Lys	ttc Phe	agt Ser 190	636
cag Gln	aaa Lys	aca Thr	agg Arg	tgg Trp 195	ttc Phe	agc Ser	ata Ile	gtc Val	cca Pro 200	tat Tyr	gaa Glu	acc Thr	aat Asn 205	aat Asn	cag Gln	684
gaa Glu	acc Thr	ttt Phe	gga Gly 210	gct Ala	ttg Leu	gac Asp	ctt Leu	ggg Gly 215	gga Gly	gcc Ala	tct Ser	aca Thr	caa Gln 220	gtc Val	act Thr	732
ttt Phe	gta Val	ccc Pro 225	caa Gln	aac Asn	cag Gln	act Thr	atc Ile 230	gag Glu	tcc Ser	cca Pro	gat Asp	aat Asn 235	gct Ala	ctg Leu	caa Gln	780
ttt Phe	cgc Arg 240	ctc Leu	tat Tyr	ggc Gly	aag Lys	gac Asp 245	tac Tyr	aat Asn	gtc Val	tac Tyr	aca Thr 250	cat His	agc Ser	ttc Phe	ttg Leu	828
tgc Cys 255	tat Tyr	ggg Gly	aag Lys	gat Asp	cag Gln 260	gca Ala	ctc Leu	tgg Trp	cag Gln	aaa Lys 265	ctg Leu	gcc Ala	aag Lys	gac Asp	att Ile 270	876
cag Gln	gtt Val	gca Ala	agt Ser	aat Asn 275	gaa Glu	att Ile	ctc Leu	agg Arg	gac Asp 280	cca Pro	tgc Cys	ttt Phe	cat His	cct Pro 285	gga Gly	924
tat Tyr	aag Lys	aag Lys	gta Val 290	gtg Val	aac Asn	gta Val	agt Ser	gac Asp 295	ctt Leu	tac Tyr	aag Lys	acc Thr	ccc Pro 300	tgc Cys	acc Thr	972
aag Lys	aga Arg	ttt Phe 305	gag Glu	atg Met	act Thr	ctt Leu	cca Pro 310	ttc Phe	cag Gln	cag Gln	ttt Phe	gaa Glu 315	atc Ile	cag Gln	ggg Gly	1020
att Ile	gga Gly 320	aac Asn	tat Tyr	caa Gln	caa Gln	tgc Cys 325	cat His	caa Gln	agc Ser	atc Ile	ctg Leu 330	gag Glu	ctc Leu	ttc Phe	aac Asn	1068
acc Thr 335	agt Ser	tac Tyr	tgc Cys	cct Pro	tac Tyr 340	tcc Ser	cag Gln	tgt Cys	gcc Ala	ttc Phe 345	aat Asn	ggg Gly	att Ile	ttc Phe	ttg Leu 350	1116
cca Pro	cca Pro	ctc Leu	cag Gln	ggg Gly 355	gat Asp	ttt Phe	ggg Gly	gca Ala	ttt Phe 360	tca Ser	gct Ala	ttt Phe	tac Tyr	ttt Phe 365	gtg Val	1164
atg Met	aag Lys	ttt Phe	tta Leu 370	aac Asn	ttg Leu	aca Thr	tca Ser	gag Glu 375	aaa Lys	gtc Val	tct Ser	cag Gln	gaa Glu 380	aag Lys	gtg Val	1212
act	gag	atg	atg	aaa	aag	ttc	tgt	gct	cag	cct 2	tgg	gag	gag	ata	aaa	1260

Thr	Glu	Met	Met	Lys	Lys	Phe	Cys	Ala	Gln	Pro	Trp	Glu	Glu	Ile	Lys		
		385					390					395					
aca	tct	tac	gct	gga	gta	aag	gag	aag	tac	ctg	agt	gaa	tac	tgc	ttt	1308	
Thr	Ser	Tyr	Ala	Gly	Val	Lys	Glu	Lys	Tyr	Leu	Ser	Glu	Tyr	Cys	Phe		
	400					405				410							
tct	ggt	acc	tac	att	ctc	tcc	ctc	ctt	ctg	caa	ggc	tat	cat	ttc	aca	1356	
Ser	Gly	Thr	Tyr	Ile	Leu	Ser	Leu	Leu	Leu	Gln	Gly	Tyr	His	Phe	Thr		
	415				420					425					430		
gct	gat	tcc	tgg	gag	cac	atc	cat	ttc	att	ggc	aag	atc	cag	ggc	agc	1404	
Ala	Asp	Ser	Trp	Glu	His	Ile	His	Phe	Ile	Gly	Lys	Ile	Gln	Gly	Ser		
				435					440					445			
gac	gcc	ggc	tgg	act	ttg	ggc	tac	atg	ctg	aac	ctg	acc	aac	atg	atc	1452	
Asp	Ala	Gly	Trp	Thr	Leu	Gly	Tyr	Met	Leu	Asn	Leu	Thr	Asn	Met	Ile		
			450					455					460				
cca	gct	gag	caa	cca	ttg	tcc	aca	cct	ctc	tcc	cac	tcc	acc	tat	gtc	1500	
Pro	Ala	Glu	Gln	Pro	Leu	Ser	Thr	Pro	Leu	Ser	His	Ser	Thr	Tyr	Val		
		465					470					475					
ttc	ctc	atg	gtt	cta	ttc	tcc	ctg	gtc	ctt	ttc	aca	gtg	gcc	atc	ata	1548	
Phe	Leu	Met	Val	Leu	Phe	Ser	Leu	Val	Leu	Phe	Thr	Val	Ala	Ile	Ile		
	480					485					490						
ggc	ttg	ctt	atc	ttt	cac	aag	cct	tca	tat	ttc	tgg	aaa	gat	atg	gta	1596	
Gly	Leu	Leu	Ile	Phe	His	Lys	Pro	Ser	Tyr	Phe	Trp	Lys	Asp	Met	Val		
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tag																1599	

<210> 2  
 <211> 510  
 <212> PRT  
 <213> Homo sapiens

<400> 2  
 Met Glu Asp Thr Lys Glu Ser Asn Val Lys Thr Phe Cys Ser Lys Asn  
 1 5 10 15  
 Ile Leu Ala Ile Leu Gly Phe Ser Ser Ile Ile Ala Val Ile Ala Leu  
 20 25 30  
 Leu Ala Val Gly Leu Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys  
 35 40 45  
 Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile  
 50 55 60  
 Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His Gln  
 65 70 75 80  
 Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln  
 85 90 95  
 Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala  
 100 105 110  
 Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu  
 115 120 125  
 Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu  
 130 135 140  
 Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro  
 145 150 155 160  
 3

Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala  
165 170 175  
Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys  
180 185 190  
Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr  
195 200 205  
Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val  
210 215 220  
Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg  
225 230 235 240  
Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr  
245 250 255  
Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val  
260 265 270  
Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys  
275 280 285  
Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg  
290 295 300  
Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly  
305 310 315 320  
Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser  
325 330 335  
Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro  
340 345 350  
Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val Met Lys  
355 360 365  
Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu  
370 375 380  
Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser  
385 390 395 400  
Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly  
405 410 415  
Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp  
420 425 430  
Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala  
435 440 445  
Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala  
450 455 460  
Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr Tyr Val Phe Leu  
465 470 475 480  
Met Val Leu Phe Ser Leu Val Leu Phe Thr Val Ala Ile Ile Gly Leu  
485 490 495  
Leu Ile Phe His Lys Pro Ser Tyr Phe Trp Lys Asp Met Val  
500 505 510

<211> 476  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Fusion  
 construct of human CD39

<400> 3  
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 Val Cys Ser Ala Val Ser His Arg Asn Gln Gln Thr Trp Phe Glu Gly  
 20 25 30  
 Ile Phe Leu Ser Ser Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys  
 35 40 45  
 Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile  
 50 55 60  
 Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His Gln  
 65 70 75 80  
 Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln  
 85 90 95  
 Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala  
 100 105 110  
 Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu  
 115 120 125  
 Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu  
 130 135 140  
 Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro  
 145 150 155 160  
 Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala  
 165 170 175  
 Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys  
 180 185 190  
 Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr  
 195 200 205  
 Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val  
 210 215 220  
 Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg  
 225 230 235 240  
 Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr  
 245 250 255  
 Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val  
 260 265 270  
 Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys  
 275 280 285  
 Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg  
 290 295 300  
 Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly  
 305 310 315 320

Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser  
 325 330 335  
 Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro  
 340 345 350  
 Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val Met Lys  
 355 360 365  
 Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu  
 370 375 380  
 Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser  
 385 390 395 400  
 Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly  
 405 410 415  
 Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp  
 420 425 430  
 Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala  
 435 440 445  
 Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala  
 450 455 460  
 Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr  
 465 470 475

<210> 4

<211> 476

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion  
construct of human CD39

<220>

<221> VARIANT

<222> (39)

<223> Any amino acid, preferably Cys or Ser

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 20 25 30  
 Ile Phe Leu Ser Ser Met Xaa Pro Ile Asn Val Ser Ala Ser Thr Leu  
 35 40 45  
 Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile  
 50 55 60  
 Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His Gln  
 65 70 75 80  
 Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln  
 85 90 95  
 Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala  
 100 105 110  
 Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu  
 115 120 125

Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu  
 130 135 140  
 Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro  
 145 150 155 160  
 Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala  
 165 170 175  
 Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys  
 180 185 190  
 Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr  
 195 200 205  
 Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val  
 210 215 220  
 Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg  
 225 230 235 240  
 Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr  
 245 250 255  
 Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val  
 260 265 270  
 Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys  
 275 280 285  
 Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg  
 290 295 300  
 Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly  
 305 310 315 320  
 Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser  
 325 330 335  
 Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro  
 340 345 350  
 Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val Met Lys  
 355 360 365  
 Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu  
 370 375 380  
 Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser  
 385 390 395 400  
 Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly  
 405 410 415  
 Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp  
 420 425 430  
 Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala  
 435 440 445  
 Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala  
 450 455 460  
 Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr  
 465 470 475

<210> 5  
 <211> 1365  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Fusion  
 construct of human CD39

<220>  
 <221> CDS  
 <222> (1)..(1362)

<400> 5  
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 Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Thr Ser Ser Thr  
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 cag aac aaa gca ttg cca gaa aac gtt aag tat ggg att gtg ctg gat 96  
 Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu Asp  
 20 25 30  
 gcg ggt tct tct cac aca agt tta tac atc tat aag tgg cca gca gaa 144  
 Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala Glu  
 35 40 45  
 aag gag aat gac aca ggc gtg gtg cat caa gta gaa gaa tgc agg gtt 192  
 Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg Val  
 50 55 60  
 aaa ggt cct gga atc tca aaa ttt gtt cag aaa gta aat gaa ata ggc 240  
 Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn Glu Ile Gly  
 65 70 75 80  
 att tac ctg act gat tgc atg gaa aga gct agg gaa gtg att cca agg 288  
 Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu Val Ile Pro Arg  
 85 90 95  
 tcc cag cac caa gag aca ccc gtt tac ctg gga gcc acg gca ggc atg 336  
 Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly Met  
 100 105 110  
 cgg ttg ctc agg atg gaa agt gaa gag ttg gca gac agg gtt ctg gat 384  
 Arg Leu Leu Arg Met Glu Ser Glu Glu Leu Ala Asp Arg Val Leu Asp  
 115 120 125  
 gtg gtg gag agg agc ctc agc aac tac ccc ttt gac ttc cag ggt gcc 432  
 Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly Ala  
 130 135 140  
 agg atc att act ggc caa gag gaa ggt gcc tat ggc tgg att act atc 480  
 Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp Ile Thr Ile  
 145 150 155 160  
 aac tat ctg ctg ggc aaa ttc agt cag aaa aca agg tgg ttc agc ata 528  
 Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Thr Arg Trp Phe Ser Ile  
 165 170 175  
 gtc cca tat gaa acc aat aat cag gaa acc ttt gga gct ttg gac ctt 576  
 Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr Phe Gly Ala Leu Asp Leu  
 180 185 190  
 ggg gga gcc tct aca caa gtc act ttt gta ccc caa aac cag act atc 624  
 Gly Gly Ala Ser Thr Gln Val Thr Phe Val Pro Gln Asn Gln Thr Ile  
 195 200 205  
 gag tcc cca gat aat gct ctg caa ttt cgc ctc tat ggc aag gac tac 672  
 Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu Tyr Gly Lys Asp Tyr  
 210 215 220



aat gtc tac aca cat agc ttc ttg tgc tat ggg aag gat cag gca ctc	720
Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly Lys Asp Gln Ala Leu	
225 230 235 240	
tg g cag aaa ctg gcc aag gac att cag gtt gca agt aat gaa att ctc	768
Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala Ser Asn Glu Ile Leu	
245 250 255	
agg gac cca tgc ttt cat cct gga tat aag aag gta gtg aac gta agt	816
Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys Val Val Asn Val Ser	
260 265 270	
gac ctt tac aag acc ccc tgc acc aag aga ttt gag atg act ctt cca	864
Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe Glu Met Thr Leu Pro	
275 280 285	
ttc cag cag ttt gaa atc cag ggt att gga aac tat caa caa tgc cat	912
Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn Tyr Gln Gln Cys His	
290 295 300	
caa agc atc ctg gag ctc ttc aac acc agt tac tgc cct tac tcc cag	960
Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr Cys Pro Tyr Ser Gln	
305 310 315 320	
tgt gcc ttc aat ggg att ttc ttg cca cca ctc cag ggg gat ttt ggg	1008
Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu Gln Gly Asp Phe Gly	
325 330 335	
gca ttt tca gct ttt tac ttt gtg atg aag ttt tta aac ttg aca tca	1056
Ala Phe Ser Ala Phe Tyr Phe Val Met Lys Phe Leu Asn Leu Thr Ser	
340 345 350	
gag aaa gtc tct cag gaa aag gtg act gag atg atg aaa aag ttc tgt	1104
Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met Met Lys Lys Phe Cys	
355 360 365	
gct cag cct tgg gag gag ata aaa aca tct tac gct gga gta aag gag	1152
Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr Ala Gly Val Lys Glu	
370 375 380	
aag tac ctg agt gaa tac tgc ttt tct ggt acc tac att ctc tcc ctc	1200
Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr Tyr Ile Leu Ser Leu	
385 390 395 400	
ctt ctg caa ggc tat cat ttc aca gct gat tcc tgg gag cac atc cat	1248
Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser Trp Glu His Ile His	
405 410 415	
ttc att ggc aag atc cag ggc agc gac gcc ggc tgg act ttg ggc tac	1296
Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly Trp Thr Leu Gly Tyr	
420 425 430	
atg ctg aac ctg acc aac atg atc cca gct gag caa cca ttg tcc aca	1344
Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu Gln Pro Leu Ser Thr	
435 440 445	
cct ctc tcc cac tcc acc taa	1365
Pro Leu Ser His Ser Thr	
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<210> 6

<211> 454

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion

construct of human CD39

<400> 6  
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Gln Asn Lys Ala<sub>20</sub> Leu Pro Glu Asn Val<sub>25</sub> Lys Tyr Gly Ile Val<sub>30</sub> Leu Asp  
Ala Gly Ser<sub>35</sub> Ser His Thr Ser Leu<sub>40</sub> Tyr Ile Tyr Lys Trp<sub>45</sub> Pro Ala Glu  
Lys Glu<sub>50</sub> Asn Asp Thr Gly Val<sub>55</sub> Val His Gln Val Glu<sub>60</sub> Glu Cys Arg Val  
Lys Gly<sub>65</sub> Pro Gly Ile Ser<sub>70</sub> Lys Phe Val Gln Lys<sub>75</sub> Val Asn Glu Ile Gly<sub>80</sub>  
Ile Tyr Leu Thr Asp<sub>85</sub> Cys Met Glu Arg Ala<sub>90</sub> Arg Glu Val Ile Pro<sub>95</sub> Arg  
Ser Gln His Gln<sub>100</sub> Glu Thr Pro Val Tyr<sub>105</sub> Leu Gly Ala Thr Ala<sub>110</sub> Gly Met  
Arg Leu Leu<sub>115</sub> Arg Met Glu Ser Glu<sub>120</sub> Glu Leu Ala Asp Arg<sub>125</sub> Val Leu Asp  
Val Val<sub>130</sub> Glu Arg Ser Leu Ser<sub>135</sub> Asn Tyr Pro Phe Asp<sub>140</sub> Phe Gln Gly Ala  
Arg Ile Ile Thr Gly Gln<sub>150</sub> Glu Glu Gly Ala Tyr<sub>155</sub> Gly Trp Ile Thr Ile<sub>160</sub>  
Asn Tyr Leu Leu Gly<sub>165</sub> Lys Phe Ser Gln Lys<sub>170</sub> Thr Arg Trp Phe Ser<sub>175</sub> Ile  
Val Pro Tyr Glu<sub>180</sub> Thr Asn Asn Gln Glu<sub>185</sub> Thr Phe Gly Ala Leu<sub>190</sub> Asp Leu  
Gly Gly Ala<sub>195</sub> Ser Thr Gln Val Thr<sub>200</sub> Phe Val Pro Gln Asn<sub>205</sub> Gln Thr Ile  
Glu Ser<sub>210</sub> Pro Asp Asn Ala Leu<sub>215</sub> Gln Phe Arg Leu Tyr<sub>220</sub> Gly Lys Asp Tyr  
Asn Val Tyr Thr His Ser<sub>230</sub> Phe Leu Cys Tyr Gly<sub>235</sub> Lys Asp Gln Ala Leu<sub>240</sub>  
Trp Gln Lys Leu Ala<sub>245</sub> Lys Asp Ile Gln Val<sub>250</sub> Ala Ser Asn Glu Ile<sub>255</sub> Leu  
Arg Asp Pro Cys<sub>260</sub> Phe His Pro Gly Tyr<sub>265</sub> Lys Lys Val Val<sub>270</sub> Asn Val Ser  
Asp Leu Tyr<sub>275</sub> Lys Thr Pro Cys Thr<sub>280</sub> Lys Arg Phe Glu Met<sub>285</sub> Thr Leu Pro  
Phe Gln Gln Phe Glu Ile Gln<sub>295</sub> Gly Ile Gly Asn Tyr<sub>300</sub> Gln Gln Cys His  
Gln Ser Ile Leu Glu Leu<sub>310</sub> Phe Asn Thr Ser Tyr<sub>315</sub> Cys Pro Tyr Ser Gln<sub>320</sub>  
Cys Ala Phe Asn Gly<sub>325</sub> Ile Phe Leu Pro Pro<sub>330</sub> Leu Gln Gly Asp Phe<sub>335</sub> Gly  
Ala Phe Ser Ala<sub>340</sub> Phe Tyr Phe Val Met<sub>345</sub> Lys Phe Leu Asn Leu<sub>350</sub> Thr Ser

Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met Met Lys Lys Phe Cys  
 355 360 365  
 Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr Ala Gly Val Lys Glu  
 370 375 380  
 Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr Tyr Ile Leu Ser Leu  
 385 390 395 400  
 Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser Trp Glu His Ile His  
 405 410 415  
 Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly Trp Thr Leu Gly Tyr  
 420 425 430  
 Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu Gln Pro Leu Ser Thr  
 435 440 445  
 Pro Leu Ser His Ser Thr  
 450

<210> 7  
 <211> 1437  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Fusion  
 construct of human CD39

<220>  
 <221> CDS  
 <222> (1)..(1434)

<400> 7  
 atg gcc ctg tgg atc gac agg atg caa ctc ctg tct tgc att gca cta 48  
 Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu  
 1 5 10 15  
 agt ctt gca ctt gtc aca aac agt gca cct act tca agt tct aca aag 96  
 Ser Leu Ala Leu Val Thr Asn Ser Ala Pro Thr Ser Ser Ser Thr Lys  
 20 25 30  
 aaa aca cag cta act agt tca acc cag aac aaa gca ttg cca gaa aac 144  
 Lys Thr Gln Leu Thr Ser Ser Thr Gln Asn Lys Ala Leu Pro Glu Asn  
 35 40 45  
 gtt aag tat ggg att gtg ctg gat gcg ggt tct tct cac aca agt tta 192  
 Val Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu  
 50 55 60  
 tac atc tat aag tgg cca gca gaa aag gag aat gac aca ggc gtg gtg 240  
 Tyr Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val  
 65 70 75 80  
 cat caa gta gaa gaa tgc agg gtt aaa ggt cct gga atc tca aaa ttt 288  
 His Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe  
 85 90 95  
 gtt cag aaa gta aat gaa ata ggc att tac ctg act gat tgc atg gaa 336  
 Val Gln Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu  
 100 105 110  
 aga gct agg gaa gtg att cca agg tcc cag cac caa gag aca ccc gtt 384  
 Arg Ala Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val  
 115 120 125

tac Tyr	ctg Leu 130	gga Gly	gcc Ala	acg Thr	gca Ala	ggc Gly 135	atg Met	cgg Arg	ttg Leu	ctc Leu	agg Arg 140	atg Met	gaa Glu	agt Ser	gaa Glu	432
gag Glu 145	ttg Leu	gca Ala	gac Asp	agg Arg	gtt Val 150	ctg Leu	gat Asp	gtg Val	gtg Val	gag Glu 155	agg Arg	agc Ser	ctc Leu	agc Ser	aac Asn 160	480
tac Tyr	ccc Pro	ttt Phe	gac Asp	ttc Phe 165	cag Gln	ggg Gly	gcc Ala	agg Arg	atc Ile 170	att Ile	act Thr	ggc Gly	caa Gln	gag Glu 175	gaa Glu	528
ggt Gly	gcc Ala	tat Tyr	ggc Gly 180	tgg Trp	att Ile	act Thr	atc Ile	aac Asn 185	tat Tyr	ctg Leu	ctg Leu	ggc Gly	aaa Lys 190	ttc Phe	agt Ser	576
cag Gln	aaa Lys	aca Thr 195	agg Arg	tgg Trp	ttc Phe	agc Ser	ata Ile 200	gtc Val	cca Pro	tat Tyr	gaa Glu	acc Thr 205	aat Asn	aat Asn	cag Gln	624
gaa Glu	acc Thr 210	ttt Phe	gga Gly	gct Ala	ttg Leu	gac Asp 215	ctt Leu	ggg Gly	gga Gly	gcc Ala	tct Ser 220	aca Thr	caa Gln	gtc Val	act Thr	672
ttt Phe 225	gta Val	ccc Pro	caa Gln	aac Asn	cag Gln 230	act Thr	atc Ile	gag Glu	tcc Ser	cca Pro 235	gat Asp	aat Asn	gct Ala	ctg Leu	caa Gln 240	720
ttt Phe	cgc Arg	ctc Leu	tat Tyr	ggc Gly 245	aag Lys	gac Asp	tac Tyr	aat Asn	gtc Val 250	tac Tyr	aca Thr	cat His	agc Ser	ttc Phe 255	ttg Leu	768
tgc Cys	tat Tyr	ggg Gly	aag Lys 260	gat Asp	cag Gln	gca Ala	ctc Leu	tgg Trp 265	cag Gln	aaa Lys	ctg Leu	gcc Ala	aag Lys 270	gac Asp	att Ile	816
cag Gln	gtt Val	gca Ala 275	agt Ser	aat Asn	gaa Glu	att Ile	ctc Leu 280	agg Arg	gac Asp	cca Pro	tgc Cys	ttt Phe 285	cat His	cct Pro	gga Gly	864
tat Tyr	aag Lys 290	aag Lys	gta Val	gtg Val	aac Asn	gta Val 295	agt Ser	gac Asp	ctt Leu	tac Tyr	aag Lys 300	acc Thr	ccc Pro	tgc Cys	acc Thr	912
aag Lys 305	aga Arg	ttt Phe	gag Glu	atg Met	act Thr 310	ctt Leu	cca Pro	ttc Phe	cag Gln 315	cag Gln 315	ttt Phe	gaa Glu	atc Ile	cag Gln	ggt Gly 320	960
att Ile	gga Gly	aac Asn	tat Tyr	caa Gln 325	caa Gln	tgc Cys	cat His	caa Gln	agc Ser 330	atc Ile	ctg Leu	gag Glu	ctc Leu	ttc Phe 335	aac Asn	1008
acc Thr	agt Ser	tac Tyr	tgc Cys 340	cct Pro	tac Tyr	tcc Ser	cag Gln	tgt Cys 345	gcc Ala	ttc Phe	aat Asn	ggg Gly	att Ile 350	ttc Phe	ttg Leu	1056
cca Pro	cca Pro	ctc Leu 355	cag Gln	ggg Gly	gat Asp	ttt Phe	ggg Gly 360	gca Ala	ttt Phe	tca Ser	gct Ala	ttt Phe 365	tac Tyr	ttt Phe	gtg Val	1104
atg Met	aag Lys 370	ttt Phe	tta Leu	aac Asn	ttg Leu	aca Thr 375	tca Ser	gag Glu	aaa Lys	gtc Val	tct Ser 380	cag Gln	gaa Glu	aag Lys	gtg Val	1152
act Thr 385	gag Glu	atg Met	atg Met	aaa Lys	aag Lys 390	ttc Phe	tgt Cys	gct Ala	cag Gln	cct Pro 395	tgg Trp	gag Glu	gag Glu	ata Ile	aaa Lys 400	1200
aca	tct	tac	gct	gga	gta	aag	gag	aag	tac	ctg 12	agt	gaa	tac	tgc	ttt	1248

Thr	Ser	Tyr	Ala	Gly	Val	Lys	Glu	Lys	Tyr	Leu	Ser	Glu	Tyr	Cys	Phe	
				405					410					415		
tct	ggt	acc	tac	att	ctc	tcc	ctc	ctt	ctg	caa	ggc	tat	cat	ttc	aca	1296
Ser	Gly	Thr	Tyr	Ile	Leu	Ser	Leu	Leu	Leu	Gln	Gly	Tyr	His	Phe	Thr	
			420					425					430			
gct	gat	tcc	tgg	gag	cac	atc	cat	ttc	att	ggc	aag	atc	cag	ggc	agc	1344
Ala	Asp	Ser	Trp	Glu	His	Ile	His	Phe	Ile	Gly	Lys	Ile	Gln	Gly	Ser	
		435					440					445				
gac	gcc	ggc	tgg	act	ttg	ggc	tac	atg	ctg	aac	ctg	acc	aac	atg	atc	1392
Asp	Ala	Gly	Trp	Thr	Leu	Gly	Tyr	Met	Leu	Asn	Leu	Thr	Asn	Met	Ile	
	450					455					460					
cca	gct	gag	caa	cca	ttg	tcc	aca	cct	ctc	tcc	cac	tcc	acc	taa		1437
Pro	Ala	Glu	Gln	Pro	Leu	Ser	Thr	Pro	Leu	Ser	His	Ser	Thr			
465					470					475						

<210> 8  
 <211> 478  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Fusion  
 construct of human CD39

<400> 8  
 Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu  
 1 5 10 15  
 Ser Leu Ala Leu Val Thr Asn Ser Ala Pro Thr Ser Ser Ser Thr Lys  
 20 25 30  
 Lys Thr Gln Leu Thr Ser Ser Thr Gln Asn Lys Ala Leu Pro Glu Asn  
 35 40 45  
 Val Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu  
 50 55 60  
 Tyr Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val  
 65 70 75 80  
 His Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe  
 85 90 95  
 Val Gln Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu  
 100 105 110  
 Arg Ala Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val  
 115 120 125  
 Tyr Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu  
 130 135 140  
 Glu Leu Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn  
 145 150 155 160  
 Tyr Pro Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu  
 165 170 175  
 Gly Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser  
 180 185 190  
 Gln Lys Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln  
 195 200 205

Glu Thr Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr  
 210 215 220  
 Phe Val Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln  
 225 230 235 240  
 Phe Arg Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu  
 245 250 255  
 Cys Tyr Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile  
 260 265 270  
 Gln Val Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly  
 275 280 285  
 Tyr Lys Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr  
 290 295 300  
 Lys Arg Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly  
 305 310 315 320  
 Ile Gly Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn  
 325 330 335  
 Thr Ser Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu  
 340 345 350  
 Pro Pro Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val  
 355 360 365  
 Met Lys Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val  
 370 375 380  
 Thr Glu Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys  
 385 390 395 400  
 Thr Ser Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe  
 405 410 415  
 Ser Gly Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr  
 420 425 430  
 Ala Asp Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser  
 435 440 445  
 Asp Ala Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile  
 450 455 460  
 Pro Ala Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr  
 465 470 475

<210> 9

<211> 24

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
signal sequence

<400> 9

Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu  
 1 5 10 15

Ser Leu Ala Leu Val Thr Asn Ser  
 20

<210> 10  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic peptide

<400> 10  
Asp Tyr Lys Asp Asp Asp Asp Lys  
1 5

<210> 11  
<211> 43  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Fusion construct of human CD39

<400> 11  
Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu  
1 5 10 15

Ser Leu Ala Leu Val Thr Asn Ser Ala Pro Thr Ser Ser Ser Thr Lys  
20 25 30

Lys Thr Gln Leu Thr Ser Ser Thr Gln Asn Lys  
35 40

<210> 12  
<211> 29  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Fusion construct of human CD39

<400> 12  
Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu  
1 5 10 15

Ser Leu Ala Leu Val Thr Asn Ser Ala Thr Gln Asn Lys  
20 25

<210> 13  
<211> 31  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Fusion construct of human CD39

<400> 13  
Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu  
1 5 10 15

Ser Leu Ala Leu Val Thr Asn Ser Ala Ser Ser Thr Gln Asn Lys  
20 25 30

[illegible]



Lys	Asp	Tyr	Lys 105	Cys	Lys	Val	Ser	Asn 110	Lys	Ala	Leu	Pro	Ala 115	Pro	Met		
cag	aaa	acc	atc	tcc	aaa	gcc	aaa	ggg	cag	ccc	cga	gaa	cca	cag	gtg	440	
Gln	Lys	Thr 120	Ile	Ser	Lys	Ala	Lys 125	Gly	Gln	Pro	Arg	Glu 130	Pro	Gln	Val		
tac	acc	ctg	ccc	cca	tcc	cgg	gat	gag	ctg	acc	aag	aac	cag	gtc	agc	488	
Tyr	Thr 135	Leu	Pro	Pro	Ser	Arg 140	Asp	Glu	Leu	Thr	Lys 145	Asn	Gln	Val	Ser		
ctg	acc	tgc	ctg	gtc	aaa	ggc	ttc	tat	ccc	agg	cac	atc	gcc	gtg	gag	536	
Leu	Thr	Cys	Leu	Val	Lys 155	Gly	Phe	Tyr	Pro	Arg 160	His	Ile	Ala	Val	Glu 165		
tgg	gag	agc	aat	ggg	cag	ccg	gag	aac	aac	tac	aag	acc	acg	cct	ccc	584	
Trp	Glu	Ser	Asn	Gly 170	Gln	Pro	Glu	Asn	Asn 175	Tyr	Lys	Thr	Thr	Pro 180	Pro		
gtg	ctg	gac	tcc	gac	ggc	tcc	ttc	ttc	ctc	tac	agc	aag	ctc	acc	gtg	632	
Val	Leu	Asp	Ser 185	Asp	Gly	Ser	Phe	Phe 190	Leu	Tyr	Ser	Lys	Leu 195	Thr	Val		
gac	aag	agc	agg	tgg	cag	cag	ggg	aac	gtc	ttc	tca	tgc	tcc	gtg	atg	680	
Asp	Lys	Ser 200	Arg	Trp	Gln	Gln	Gly 205	Asn	Val	Phe	Ser	Cys 210	Ser	Val	Met		
cat	gag	gct	ctg	cac	aac	cac	tac	acg	cag	aag	agc	ctc	tcc	ctg	tct	728	
His	Glu 215	Ala	Leu	His	Asn	His 220	Tyr	Thr	Gln	Lys	Ser 225	Leu	Ser	Leu	Ser		
ccg	ggt	aaa	tga													740	
Pro	Gly	Lys															
230																	

<210> 17  
 <211> 232  
 <212> PRT  
 <213> Homo sapiens

<400> 17

Glu	Pro	Arg	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala		
1				5					10					15			
Pro	Glu	Ala	Glu	Gly	Ala	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro		
		20						25				30					
Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val		
		35					40					45					
Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val		
	50					55					60						
Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln		
65					70					75					80		
Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln		
				85					90					95			
Asp	Trp	Leu	Asn	Gly	Lys	Asp	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala		
			100					105					110				
Leu	Pro	Ala	Pro	Met	Gln	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro		
		115					120					125					
Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr		
	130					135					140						

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Arg  
 145 150 155 160  
 His Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr  
 165 170 175  
 Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr  
 180 185 190  
 Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe  
 195 200 205  
 Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys  
 210 215 220  
 Ser Leu Ser Leu Ser Pro Gly Lys  
 225 230

<210> 18  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide

<400> 18  
 ctttccatcc tgagcaac 18

<210> 19  
 <211> 36  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide

<400> 19  
 aaaaaactag tcagaacaaa gctttgccag aaaacg 36

<210> 20  
 <211> 24  
 <212> PRT  
 <213> Mus sp.

<400> 20  
 Met Phe His Val Ser Phe Arg Tyr Ile Phe Gly Ile Pro Pro Leu Ile  
 1 5 10 15  
 Leu Val Leu Leu Pro Val Thr Ser  
 20

<210> 21  
 <211> 46  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide

<400> 21  
 ctagttctgg agactacaaa gatgacgatg acaaaaccca gaacaa 46

<210> 22  
 <211> 46  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 22  
 agctttgttc tgggttttgt catcgatc tttgtagtct ccagaa 46

<210> 23  
 <211> 89  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 23  
 ccggtggac tttgggtac atgctgaacc tgaccaacat gatcccagct gagcaaccat 60  
 tgtccacacc tctctccac tccaccta 89

<210> 24  
 <211> 89  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 24  
 ggccttaggt ggagtgggag agaggtgtgg acaatgggtg ctcagctggg atcatgttgg 60  
 tcaggttcag catgtagccc aaagtccag 89

<210> 25  
 <211> 1464  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <221> CDS  
 <222> (1)..(1461)

<220>  
 <223> Description of Artificial Sequence: Fusion construct of human CD39

<400> 25  
 atg gcc ctg tgg atc gac agg atg caa ctc ctg tct tgc att gca cta 48  
 Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu  
 1 5 10 15

agt ctt gca ctt gtc aca aac agt gca cct act tca agt tct aca aag 96  
 Ser Leu Ala Leu Val Thr Asn Ser Ala Pro Thr Ser Ser Ser Thr Lys  
 20 25 30

aaa Lys	aca Thr	cag Gln 35	cta Leu	act Thr	agt Ser	tca Ser	gga Gly 40	gac Asp	tac Tyr	aaa Lys	gat Asp	gac Asp 45	gat Asp	gac Asp	aaa Lys	144
acc Thr	cag Gln 50	aac Asn	aaa Lys	gca Ala	ttg Leu	cca Pro 55	gaa Glu	aac Asn	gtt Val	aag Lys	tat Tyr 60	ggg Gly	att Ile	gtg Val	ctg Leu	192
gat Asp 65	gcg Ala	ggt Gly	tct Ser	tct Ser	cac His 70	aca Thr	agt Ser	tta Leu	tac Tyr	atc Ile 75	tat Tyr	aag Lys	tgg Trp	cca Pro	gca Ala 80	240
gaa Glu	aag Lys	gag Glu	aat Asn	gac Asp 85	aca Thr	ggc Gly	gtg Val	gtg Val	cat His 90	caa Gln	gta Val	gaa Glu	gaa Glu	tgc Cys 95	agg Arg	288
gtt Val	aaa Lys	ggt Gly	cct Pro 100	gga Gly	atc Ile	tca Ser	aaa Lys	ttt Phe 105	gtt Val	cag Gln	aaa Lys	gta Val	aat Asn 110	gaa Glu	ata Ile	336
ggc Gly	att Ile	tac Tyr 115	ctg Leu	act Thr	gat Asp	tgc Cys	atg Met 120	gaa Glu	aga Arg	gct Ala	agg Arg	gaa Glu 125	gtg Val	att Ile	cca Pro	384
agg Arg 130	tcc Ser	cag Gln	cac His	caa Gln	gag Glu	aca Thr 135	ccc Pro	gtt Val	tac Tyr	ctg Leu	gga Gly 140	gcc Ala	acg Thr	gca Ala	ggc Gly	432
atg Met 145	cgg Arg	ttg Leu	ctc Leu	agg Arg	atg Met 150	gaa Glu	agt Ser	gaa Glu	gag Glu	ttg Leu 155	gca Ala	gac Asp	agg Arg	gtt Val	ctg Leu 160	480
gat Asp	gtg Val	gtg Val	gag Glu	agg Arg 165	agc Ser	ctc Leu	agc Ser	aac Asn	tac Tyr 170	ccc Pro	ttt Phe	gac Asp	ttc Phe	cag Gln 175	ggc Gly	528
gcc Ala	agg Arg	atc Ile	att Ile 180	act Thr	ggc Gly	caa Gln	gag Glu	gaa Glu 185	ggt Gly	gcc Ala	tat Tyr	ggc Gly	tgg Trp 190	att Ile	act Thr	576
atc Ile	aac Asn	tat Tyr 195	ctg Leu	ctg Leu	ggc Gly	aaa Lys	ttc Phe 200	agt Ser	cag Gln	aaa Lys	aca Thr	agg Arg 205	tgg Trp	ttc Phe	agc Ser	624
ata Ile 210	gtc Val	cca Pro	tat Tyr	gaa Glu	acc Thr	aat Asn 215	aat Asn	cag Gln	gaa Glu	acc Thr	ttt Phe 220	gga Gly	gct Ala	ttg Leu	gac Asp	672
ctt Leu 225	ggg Gly	gga Gly	gcc Ala	tct Ser	aca Thr 230	caa Gln	gtc Val	act Thr	ttt Phe	gta Val 235	ccc Pro	caa Gln	aac Asn	cag Gln 240	act Thr 240	720
atc Ile	gag Glu	tcc Ser	cca Pro	gat Asp 245	aat Asn	gct Ala	ctg Leu	caa Gln	ttt Phe 250	cgc Arg	ctc Leu	tat Tyr	ggc Gly	aag Lys 255	gac Asp	768
tac Tyr	aat Asn	gtc Val	tac Tyr 260	aca Thr	cat His	agc Ser	ttc Phe	ttg Leu 265	tgc Cys	tat Tyr	ggg Gly	aag Lys	gat Asp 270	cag Gln	gca Ala	816
ctc Leu	tgg Trp	cag Gln 275	aaa Lys	ctg Leu	gcc Ala	aag Lys	gac Asp 280	att Ile	cag Gln	gtt Val	gca Ala	agt Ser 285	aat Asn	gaa Glu	att Ile	864
ctc Leu 290	agg Arg	gac Asp	cca Pro	tgc Cys	ttt Phe	cat His 295	cct Pro	gga Gly	tat Tyr	aag Lys	aag Lys 300	gta Val	gtg Val	aac Asn	gta Val	912
agt Glu	gac Glu	ctt Glu	tac Glu	aag Glu	acc Glu	ccc Glu	tgc Glu	acc Glu	aag Glu	aga Glu 20	ttt Glu	gag Glu	atg Glu	act Glu	ctt Glu	960

Ser 305	Asp	Leu	Tyr	Lys	Thr 310	Pro	Cys	Thr	Lys	Arg 315	Phe	Glu	Met	Thr	Leu 320	
cca	ttc	cag	cag	ttt	gaa	atc	cag	ggt	att	gga	aac	tat	caa	caa	tgc	1008
Pro	Phe	Gln	Gln	Phe 325	Glu	Ile	Gln	Gly	Ile 330	Gly	Asn	Tyr	Gln	Gln 335	Cys	
cat	caa	agc	atc	ctg	gag	ctc	ttc	aac	acc	agt	tac	tgc	cct	tac	tcc	1056
His	Gln	Ser	Ile 340	Leu	Glu	Leu	Phe	Asn 345	Thr	Ser	Tyr	Cys	Pro 350	Tyr	Ser	
cag	tgt	gcc	ttc	aat	ggg	att	ttc	ttg	cca	cca	ctc	cag	ggg	gat	ttt	1104
Gln	Cys	Ala 355	Phe	Asn	Gly	Ile	Phe 360	Leu	Pro	Pro	Leu	Gln 365	Gly	Asp	Phe	
ggg	gca	ttt	tca	gct	ttt	tac	ttt	gtg	atg	aag	ttt	tta	aac	ttg	aca	1152
Gly	Ala 370	Phe	Ser	Ala	Phe	Tyr 375	Phe	Val	Met	Lys	Phe 380	Leu	Asn	Leu	Thr	
tca	gag	aaa	gtc	tct	cag	gaa	aag	gtg	act	gag	atg	atg	aaa	aag	ttc	1200
Ser 385	Glu	Lys	Val	Ser	Gln 390	Glu	Lys	Val	Thr	Glu 395	Met	Met	Lys	Lys	Phe 400	
tgt	gct	cag	cct	tgg	gag	gag	ata	aaa	aca	tct	tac	gct	gga	gta	aag	1248
Cys	Ala	Gln	Pro	Trp 405	Glu	Glu	Ile	Lys	Thr 410	Ser	Tyr	Ala	Gly	Val 415	Lys	
gag	aag	tac	ctg	agt	gaa	tac	tgc	ttt	tct	ggt	acc	tac	att	ctc	tcc	1296
Glu	Lys	Tyr	Leu 420	Ser	Glu	Tyr	Cys	Phe 425	Ser	Gly	Thr	Tyr	Ile 430	Leu	Ser	
ctc	ctt	ctg	caa	ggc	tat	cat	ttc	aca	gct	gat	tcc	tgg	gag	cac	atc	1344
Leu	Leu 435	Leu	Gln	Gly	Tyr	His	Phe 440	Thr	Ala	Asp	Ser	Trp 445	Glu	His	Ile	
cat	ttc	att	ggc	aag	atc	cag	ggc	agc	gac	gcc	ggc	tgg	act	ttg	ggc	1392
His	Phe 450	Ile	Gly	Lys	Ile	Gln 455	Gly	Ser	Asp	Ala	Gly 460	Trp	Thr	Leu	Gly	
tac	atg	ctg	aac	ctg	acc	aac	atg	atc	cca	gct	gag	caa	cca	ttg	tcc	1440
Tyr 465	Met	Leu	Asn	Leu	Thr 470	Asn	Met	Ile	Pro	Ala 475	Glu	Gln	Pro	Leu	Ser 480	
aca	cct	ctc	tcc	cac	tcc	acc	taa									1464
Thr	Pro	Leu	Ser	His 485	Ser	Thr										

<210> 26  
 <211> 487  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Fusion  
 construct of human CD39

<400> 26  
 Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu  
 1 5 10 15  
 Ser Leu Ala Leu Val Thr Asn Ser Ala Pro Thr Ser Ser Ser Thr Lys  
 20 25 30  
 Lys Thr Gln Leu Thr Ser Ser Gly Asp Tyr Lys Asp Asp Asp Lys  
 35 40 45  
 Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu  
 50 55 60

Asp<sub>65</sub> Ala Gly Ser Ser His<sub>70</sub> Thr Ser Leu Tyr Ile<sub>75</sub> Tyr Lys Trp Pro Ala<sub>80</sub>  
 Glu Lys Glu Asn Asp<sub>85</sub> Thr Gly Val Val His<sub>90</sub> Gln Val Glu Glu Cys<sub>95</sub> Arg  
 Val Lys Gly Pro<sub>100</sub> Gly Ile Ser Lys Phe<sub>105</sub> Val Gln Lys Val Asn<sub>110</sub> Glu Ile  
 Gly Ile Tyr<sub>115</sub> Leu Thr Asp Cys Met<sub>120</sub> Glu Arg Ala Arg Glu<sub>125</sub> Val Ile Pro  
 Arg Ser<sub>130</sub> Gln His Gln Glu Thr<sub>135</sub> Pro Val Tyr Leu Gly<sub>140</sub> Ala Thr Ala Gly  
 Met<sub>145</sub> Arg Leu Leu Arg Met<sub>150</sub> Glu Ser Glu Glu Leu<sub>155</sub> Ala Asp Arg Val Leu<sub>160</sub>  
 Asp Val Val Glu Arg<sub>165</sub> Ser Leu Ser Asn Tyr<sub>170</sub> Pro Phe Asp Phe Gln<sub>175</sub> Gly  
 Ala Arg Ile Ile<sub>180</sub> Thr Gly Gln Glu Glu<sub>185</sub> Gly Ala Tyr Gly Trp<sub>190</sub> Ile Thr  
 Ile Asn Tyr<sub>195</sub> Leu Leu Gly Lys Phe<sub>200</sub> Ser Gln Lys Thr Arg<sub>205</sub> Trp Phe Ser  
 Ile Val<sub>210</sub> Pro Tyr Glu Thr Asn<sub>215</sub> Asn Gln Glu Thr Phe<sub>220</sub> Gly Ala Leu Asp  
 Leu<sub>225</sub> Gly Gly Ala Ser Thr<sub>230</sub> Gln Val Thr Phe Val<sub>235</sub> Pro Gln Asn Gln Thr<sub>240</sub>  
 Ile Glu Ser Pro Asp<sub>245</sub> Asn Ala Leu Gln Phe<sub>250</sub> Arg Leu Tyr Gly Lys<sub>255</sub> Asp  
 Tyr Asn Val Tyr<sub>260</sub> Thr His Ser Phe Leu<sub>265</sub> Cys Tyr Gly Lys Asp<sub>270</sub> Gln Ala  
 Leu Trp Gln<sub>275</sub> Lys Leu Ala Lys Asp<sub>280</sub> Ile Gln Val Ala Ser<sub>285</sub> Asn Glu Ile  
 Leu Arg<sub>290</sub> Asp Pro Cys Phe His<sub>295</sub> Pro Gly Tyr Lys Lys<sub>300</sub> Val Val Asn Val  
 Ser<sub>305</sub> Asp Leu Tyr Lys Thr<sub>310</sub> Pro Cys Thr Lys Arg<sub>315</sub> Phe Glu Met Thr Leu<sub>320</sub>  
 Pro Phe Gln Gln Phe<sub>325</sub> Glu Ile Gln Gly Ile<sub>330</sub> Gly Asn Tyr Gln Gln<sub>335</sub> Cys  
 His Gln Ser Ile<sub>340</sub> Leu Glu Leu Phe Asn<sub>345</sub> Thr Ser Tyr Cys Pro<sub>350</sub> Tyr Ser  
 Gln Cys Ala<sub>355</sub> Phe Asn Gly Ile Phe<sub>360</sub> Leu Pro Pro Leu Gln<sub>365</sub> Gly Asp Phe  
 Gly Ala<sub>370</sub> Phe Ser Ala Phe Tyr<sub>375</sub> Phe Val Met Lys Phe<sub>380</sub> Leu Asn Leu Thr  
 Ser<sub>385</sub> Glu Lys Val Ser Gln<sub>390</sub> Glu Lys Val Thr Glu<sub>395</sub> Met Met Lys Lys Phe<sub>400</sub>  
 Cys Ala Gln Pro Trp<sub>405</sub> Glu Glu Ile Lys Thr<sub>410</sub> Ser Tyr Ala Gly Val<sub>415</sub> Lys  
 Glu Lys Tyr Leu<sub>420</sub> Ser Glu Tyr Cys Phe<sub>425</sub> Ser Gly Thr Tyr Ile<sub>430</sub> Leu Ser

Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser Trp Glu His Ile  
           435                          440                          445  
 His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly Trp Thr Leu Gly  
           450                          455                          460  
 Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu Gln Pro Leu Ser  
 465                          470                          475                          480  
 Thr Pro Leu Ser His Ser Thr  
                           485

<210> 27  
 <211> 464  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Fusion  
           construct of human CD39

<400> 27  
 Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu  
   1                          5                          10                          15  
 Ser Leu Ala Leu Val Thr Asn Ser Ala Thr Gln Asn Lys Ala Leu Pro  
                           20                          25                          30  
 Glu Asn Val Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr  
           35                          40                          45  
 Ser Leu Tyr Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly  
   50                          55                          60  
 Val Val His Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser  
   65                          70                          75                          80  
 Lys Phe Val Gln Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys  
                           85                          90                          95  
 Met Glu Arg Ala Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr  
                           100                          105                          110  
 Pro Val Tyr Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu  
           115                          120                          125  
 Ser Glu Glu Leu Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu  
   130                          135                          140  
 Ser Asn Tyr Pro Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln  
 145                          150                          155                          160  
 Glu Glu Gly Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys  
           165                          170  
 Phe Ser Gln Lys Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn  
           180                          185                          190  
 Asn Gln Glu Thr Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln  
           195                          200                          205  
 Val Thr Phe Val Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala  
   210                          215                          220  
 Leu Gln Phe Arg Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser  
 225                          230                          235                          240  
   23





Trp<sub>65</sub> Pro Ala Glu Lys Glu<sub>70</sub> Asn Asp Thr Gly Val<sub>75</sub> Val His Gln Val Glu<sub>80</sub>  
 Glu Cys Arg Val Lys<sub>85</sub> Gly Pro Gly Ile Ser<sub>90</sub> Lys Phe Val Gln Lys<sub>95</sub> Val  
 Asn Glu Ile Gly<sub>100</sub> Ile Tyr Leu Thr Asp<sub>105</sub> Cys Met Glu Arg Ala<sub>110</sub> Arg Glu  
 Val Ile Pro<sub>115</sub> Arg Ser Gln His Gln<sub>120</sub> Glu Thr Pro Val Tyr<sub>125</sub> Leu Gly Ala  
 Thr Ala<sub>130</sub> Gly Met Arg Leu Leu<sub>135</sub> Arg Met Glu Ser Glu<sub>140</sub> Glu Leu Ala Asp  
 Arg Val Leu Asp Val Val<sub>150</sub> Glu Arg Ser Leu Ser<sub>155</sub> Asn Tyr Pro Phe Asp<sub>160</sub>  
 Phe Gln Gly Ala Arg<sub>165</sub> Ile Ile Thr Gly Gln<sub>170</sub> Glu Glu Gly Ala Tyr<sub>175</sub> Gly  
 Trp Ile Thr Ile<sub>180</sub> Asn Tyr Leu Leu Gly<sub>185</sub> Lys Phe Ser Gln Lys<sub>190</sub> Thr Arg  
 Trp Phe Ser<sub>195</sub> Ile Val Pro Tyr Glu<sub>200</sub> Thr Asn Asn Gln Glu<sub>205</sub> Thr Phe Gly  
 Ala Leu<sub>210</sub> Asp Leu Gly Gly Ala<sub>215</sub> Ser Thr Gln Val Thr<sub>220</sub> Phe Val Pro Gln  
 Asn Gln Thr Ile Glu Ser<sub>230</sub> Pro Asp Asn Ala Leu<sub>235</sub> Gln Phe Arg Leu Tyr<sub>240</sub>  
 Gly Lys Asp Tyr Asn<sub>245</sub> Val Tyr Thr His Ser<sub>250</sub> Phe Leu Cys Tyr Gly<sub>255</sub> Lys  
 Asp Gln Ala Leu<sub>260</sub> Trp Gln Lys Leu Ala<sub>265</sub> Lys Asp Ile Gln Val<sub>270</sub> Ala Ser  
 Asn Glu Ile<sub>275</sub> Leu Arg Asp Pro Cys<sub>280</sub> Phe His Pro Gly Tyr<sub>285</sub> Lys Lys Val  
 Val Asn Val Ser Asp Leu Tyr<sub>295</sub> Lys Thr Pro Cys Thr<sub>300</sub> Lys Arg Phe Glu  
 Met Thr Leu Pro Phe Gln<sub>310</sub> Gln Phe Glu Ile Gln<sub>315</sub> Gly Ile Gly Asn Tyr<sub>320</sub>  
 Gln Gln Cys His Gln<sub>325</sub> Ser Ile Leu Glu Leu<sub>330</sub> Phe Asn Thr Ser Tyr<sub>335</sub> Cys  
 Pro Tyr Ser Gln<sub>340</sub> Cys Ala Phe Asn Gly<sub>345</sub> Ile Phe Leu Pro Pro<sub>350</sub> Leu Gln  
 Gly Asp Phe<sub>355</sub> Gly Ala Phe Ser Ala<sub>360</sub> Phe Tyr Phe Val Met<sub>365</sub> Lys Phe Leu  
 Asn Leu<sub>370</sub> Thr Ser Glu Lys Val<sub>375</sub> Ser Gln Glu Lys Val<sub>380</sub> Thr Glu Met Met  
 Lys<sub>385</sub> Lys Phe Cys Ala Gln<sub>390</sub> Pro Trp Glu Glu Ile<sub>395</sub> Lys Thr Ser Tyr Ala<sub>400</sub>  
 Gly Val Lys Glu Lys<sub>405</sub> Tyr Leu Ser Glu Tyr<sub>410</sub> Cys Phe Ser Gly Thr<sub>415</sub> Tyr  
 Ile Leu Ser Leu<sub>420</sub> Leu Leu Gln Gly Tyr<sub>425</sub> His Phe Thr Ala Asp<sub>430</sub> Ser Trp

Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly Trp  
435 445  
Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu Gln  
450 455 460  
Pro Leu Ser Thr Pro Leu Ser His Ser Thr  
465 470

<210> 29  
<211> 473  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Fusion  
construct of human CD39

<400> 29  
Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu  
1 5 10 15  
Ser Leu Ala Leu Val Thr Asn Ser Ser Thr Lys Lys Thr Gln Leu Thr  
20 25 30  
Ser Ser Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile  
35 40 45  
Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp  
50 55 60  
Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu  
65 70 75 80  
Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn  
85 90 95  
Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu Val  
100 105 110  
Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr  
115 120 125  
Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu Ala Asp Arg  
130 135 140  
Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe  
145 150 155 160  
Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp  
165 170 175  
Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Thr Arg Trp  
180 185 190  
Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr Phe Gly Ala  
195 200 205  
Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val Pro Gln Asn  
210 215 220  
Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu Tyr Gly  
225 230 235 240  
Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly Lys Asp  
245 250 255

Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala Ser Asn  
 260 265 270  
 Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys Val Val  
 275 280 285  
 Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe Glu Met  
 290 295 300  
 Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn Tyr Gln  
 305 310 315 320  
 Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr Cys Pro  
 325 330 335  
 Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu Gln Gly  
 340 345 350  
 Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val Met Lys Phe Leu Asn  
 355 360 365  
 Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met Met Lys  
 370 375 380  
 Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr Ala Gly  
 385 390 395 400  
 Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr Tyr Ile  
 405 410 415  
 Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser Trp Glu  
 420 425 430  
 His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly Trp Thr  
 435 440 445  
 Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu Gln Pro  
 450 455 460  
 Leu Ser Thr Pro Leu Ser His Ser Thr  
 465 470

<210> 30  
 <211> 463  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Fusion  
 construct of human CD39

<400> 30  
 Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro  
 1 5 10 15  
 Gly Ser Thr Gly Ala Pro Thr Ser Thr Gln Asn Lys Ala Leu Pro Glu  
 20 25 30  
 Asn Val Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser  
 35 40 45  
 Leu Tyr Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val  
 50 55 60  
 Val His Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys  
 65 70 75 80

Phe Val Gln Lys Val<sub>85</sub> Asn Glu Ile Gly Ile<sub>90</sub> Tyr Leu Thr Asp Cys<sub>95</sub> Met  
Glu Arg Ala Arg<sub>100</sub> Glu Val Ile Pro Arg<sub>105</sub> Ser Gln His Gln<sub>110</sub> Thr Pro  
Val Tyr Leu<sub>115</sub> Gly Ala Thr Ala Gly<sub>120</sub> Met Arg Leu Leu Arg<sub>125</sub> Met Glu Ser  
Glu Glu<sub>130</sub> Leu Ala Asp Arg Val<sub>135</sub> Leu Asp Val Val<sub>140</sub> Glu Arg Ser Leu Ser  
Asn Tyr Pro Phe Asp Phe<sub>150</sub> Gln Gly Ala Arg Ile<sub>155</sub> Ile Thr Gly Gln Glu<sub>160</sub>  
Glu Gly Ala Tyr Gly<sub>165</sub> Trp Ile Thr Ile Asn<sub>170</sub> Tyr Leu Leu Gly Lys<sub>175</sub> Phe  
Ser Gln Lys Thr<sub>180</sub> Arg Trp Phe Ser Ile<sub>185</sub> Val Pro Tyr Glu Thr<sub>190</sub> Asn Asn  
Gln Glu Thr<sub>195</sub> Phe Gly Ala Leu Asp<sub>200</sub> Leu Gly Gly Ala Ser<sub>205</sub> Thr Gln Val  
Thr Phe<sub>210</sub> Val Pro Gln Asn Gln<sub>215</sub> Thr Ile Glu Ser Pro<sub>220</sub> Asp Asn Ala Leu  
Gln Phe Arg Leu Tyr Gly<sub>230</sub> Lys Asp Tyr Asn Val<sub>235</sub> Tyr Thr His Ser Phe<sub>240</sub>  
Leu Cys Tyr Gly Lys<sub>245</sub> Asp Gln Ala Leu Trp<sub>250</sub> Gln Lys Leu Ala Lys<sub>255</sub> Asp  
Ile Gln Val Ala<sub>260</sub> Ser Asn Glu Ile Leu<sub>265</sub> Arg Asp Pro Cys Phe<sub>270</sub> His Pro  
Gly Tyr Lys<sub>275</sub> Lys Val Val Asn Val<sub>280</sub> Ser Asp Leu Tyr Lys<sub>285</sub> Thr Pro Cys  
Thr Lys<sub>290</sub> Arg Phe Glu Met Thr<sub>295</sub> Leu Pro Phe Gln Gln<sub>300</sub> Phe Glu Ile Gln  
Gly Ile Gly Asn Tyr Gln<sub>310</sub> Gln Cys His Gln Ser<sub>315</sub> Ile Leu Glu Leu Phe<sub>320</sub>  
Asn Thr Ser Tyr Cys<sub>325</sub> Pro Tyr Ser Gln Cys<sub>330</sub> Ala Phe Asn Gly Ile<sub>335</sub> Phe  
Leu Pro Pro Leu<sub>340</sub> Gln Gly Asp Phe Gly<sub>345</sub> Ala Phe Ser Ala Phe<sub>350</sub> Tyr Phe  
Val Met Lys<sub>355</sub> Phe Leu Asn Leu Thr<sub>360</sub> Ser Glu Lys Val Ser<sub>365</sub> Gln Glu Lys  
Val Thr<sub>370</sub> Glu Met Met Lys Lys<sub>375</sub> Phe Cys Ala Gln Pro<sub>380</sub> Trp Glu Glu Ile  
Lys Thr Ser Tyr Ala Gly<sub>390</sub> Val Lys Glu Lys Tyr<sub>395</sub> Leu Ser Glu Tyr Cys<sub>400</sub>  
Phe Ser Gly Thr Tyr<sub>405</sub> Ile Leu Ser Leu Leu<sub>410</sub> Leu Gln Gly Tyr His<sub>415</sub> Phe  
Thr Ala Asp Ser<sub>420</sub> Trp Glu His Ile His<sub>425</sub> Phe Ile Gly Lys Ile<sub>430</sub> Gln Gly  
Ser Asp Ala Gly Trp Thr Leu Gly<sub>440</sub> Tyr Met Leu Asn Leu<sub>445</sub> Thr Asn Met

Ile Pro Ala Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr  
 450 455 460

<210> 31  
 <211> 58  
 <212> PRT  
 <213> Homo sapiens

<400> 31  
 Met Ala Thr Ser Trp Gly Thr val Phe Phe Met Leu val val ser cys  
 1 5 10 15

val cys ser ala val ser his arg asn gln gln thr trp phe glu gly  
 20 25 30

Ile phe leu ser ser met cys pro ile asn val ser ala ser thr leu  
 35 40 45

tyr gly ile met phe asp ala gly ser thr  
 50 55

<210> 32  
 <211> 11  
 <212> PRT  
 <213> artificial

<220>  
 <223> linker sequence

<400> 32

gly gly gly gly ser gly gly gly gly gly ser  
 1 5 10

<210> 33  
 <211> 13  
 <212> PRT  
 <213> artificial

<220>  
 <223> linker sequence

<400> 33

gly ala gly gly ala gly ser gly gly gly gly gly ser  
 1 5 10

<210> 34  
 <211> 10  
 <212> PRT  
 <213> artificial

<220>  
 <223> linker sequence

<400> 34

gly gly gly gly ser gly gly gly gly ser  
 1 5 10

<210> 35  
 <211> 9  
 <212> PRT  
 <213> artificial

<220>

<223> linker sequence

<400> 35

Gly Thr Pro Gly Thr Pro Gly Thr Pro  
1 5

<210> 36

<211> 26

<212> PRT

<213> artificial

<220>

<223> linker sequence

<400> 36

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly  
1 5 10 15

Gly Gly Gly Ser Gly Gly Gly Gly Gly Ser  
20 25

<210> 37

<211> 4

<212> PRT

<213> artificial

<220>

<223> linker sequence

<400> 37

Thr Ser Ser Gly  
1